We claim:

1. A method of decreasing infection of a host cell by a virus, comprising interfering with an activity or expression of one or more host proteins or interfering with an activity of one or more host nucleic acids, wherein the host protein or host nucleic acid is a T-cell receptor V beta chain; T-cell receptor V-D-J beta 2.1 chain; β-chimerin; malic enzyme 1; hypothetical protein XP_174419; sequence from chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III (F3); LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine nucleotide exchange factor 4, isoform a; APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4; v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins (LOC57826); LOC161005; osteoblast specific factor 2; Canis familiaris T-cell leukemia translocation-associated protein; aminomethyltransferase; dystroglycan; bassoon; LIM domain containing preferred translocation partner in lipoma; sequence between LOC253121 and hyaluronan synthase 2; testin 2, testin 3; protein tyrosine phosphatase, non-receptor type 1; sequence between LOC149360 and LOC253961; sequence between KIAA1560 and tectorin beta; cadherin related 23; myeloid/lymphoma or mixed lineage leukemia, translocated to 10; exportin 5; DNA polymerase eta (POLH); heterogenous nuclear riboprotein C (C1/C2); alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9 (FLJ10402); T-cell receptor beta; similar to murine putative transcription factor ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773; similar to ribosomal protein L24-like (LOC149360); polybromo 1; DNA damage inducible transcript 3; KIAA1887; PDZ ; LIM domain 1 (elfin); LOC284803; PRO0097; FLJ31958; small inducible cytokine E, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase (SMURF2); MGC40489; Rab9; PRO1617; retinoblastoma binding protein 1; region of chromosome 2q12; elongation factor for selenoprotein translation; Transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5 (TNRC5); homogentisate 1,2-dioxygenase (HGD); region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4, including UPS9X; LOC221829 ; U3 small nuclear RNA; integrin, beta 1 (ITGB1) ; acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein and FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7); Mus musculus 5S rRNA pseudogene (Rn5s-ps1); ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome cell adhesion molecule like 1 (DSCAML1); LOC148529; Huntingtin-associated protein interacting protein (HAPIP); LOC158525

and similar to RIKEN cDNA 1210001E11 (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2); C10orf7; LOC346658 and LOC340349; region of chromosome 12q21; LOC339248 and FLJ22659; SR rich protein DKFZp564B0769 and hypothetical protein MGC14793; FLJ10439; cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A; ribosomal protein S16 (RPS16); hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY); calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK); cyclin M2 (CNNM2); or AXL receptor tyrosine kinase (AXL), and wherein interfering with the activity or expression of the one or more host proteins decreases infection of the host cell by the virus.

2. The method of claim 1, wherein the one or more host proteins is encoded by one or more host nucleic acids comprising at least 90% identity to any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229 or 231.

3. The method of claim 2, wherein the one or more host nucleic acids comprises any target nucleic acid sequence associated with SEQ ID NOS: 1-227, 229 or 231.

4. The method of claim 1, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

5. The method of claim 1, wherein the method comprises interfering with an activity or expression of at least three of the host proteins.

6. The method of claim 1 wherein the virus is HIV-1 or HIV-2, and the host protein or host nucleic acid is a T-cell receptor V beta chain; T-cell receptor V-D-J beta 2.1 chain; β-chimerin; malic enzyme 1; hypothetical protein XP_174419; sequence from chromosome 4q31.3-32; alpha satellite DNA; LOC253788; LOC219938; coagulation factor III; LOC91759; similar to KOX4 (LOC131880); LOC166140; LOC222474; similar to Rho guanine nucleotide exchange factor 4, isoform a; APC-stimulated guanine nucleotide exchange factor (LOC221178); T-cell receptor beta; ribosomal protein L7A-like 4 (RPL7AL4); v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) (SRC); KIAA0564; alpha satellite DNA; M96 protein; hypothetical protein similar to G proteins; RAP-2A (LOC57826); LOC161005; Rab9, or osteoblast specific factor 2.

7. The method of claim 6, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

8. The method of claim 6, wherein the method comprises interfering with expression of one or more of the host nucleic acids.

9. The method of claim 1 wherein the virus is influenza A, and the host protein is a Canis familiaris T-cell leukemia translocation-associated protein, aminomethyltransferase; dystroglycan; bassoon; LIM domain containing preferred translocation partner in lipoma; sequence between LOC253121 and hyaluronan synthase 2; testin 2; testin 3; PTPN1 gene for protein tyrosine phosphatase, non-receptor type 1; sequence between LOC149360 and LOC253961; sequence between KIAA1560 and tectorin beta; cadherin related 23; malic enzyme 1; hypothetical protein XP_174419; sequence from chromosome 4q31.3-32; Rab9, or a myeloid/lymphoma or mixed lineage leukemia, translocated to 10.

10. The method of claim 9, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

11. The method of claim 9, wherein the method comprises interfering with expression of one or more of the host nucleic acids.

12. The method of claim 1 wherein the virus is Ebola, and the host protein is a exportin 5; DNA polymerase eta (POLH); heterogenous nuclear riboprotein C; alpha-endosulfine pseudogene; LOC128741; LOC222888; LOC138421; zinc finger protein 297B; sideroflexin 5; importin 9 (FLJ10402); T-cell receptor beta; similar to murine putative transcription factor ZNF131 (LOC135952); KIAA1259; MURR1; CCT4; FLJ40773; ribosomal protein L24-like (LOC149360); testin 2; testin 3; polybromo 1; DNA damage inducible transcript 3; KIAA1887; PDZ; LIM domain 1 (elfin); LOC284803; PRO0097; FLJ31958; small inducible cytokine E, member 1 (endothelial monocyte-activating); E3 ubiquitin ligase; MGC40489; Rab9; PRO1617; retinoblastoma binding protein 1; region of chromosome 2q12; elongation factor for selenoprotein translation; Transcription factor SMIF (HSA275986); KIAA1026; trinucleotide repeat containing 5 (TNRC5); homogentisate 1,2-dioxygenase (HGD); region of chromosome Xq23-24; region of chromosome 4p15.3; similar to LWamide neuropeptide precursor protein [Hydractinia echinata] (LOC129883); region of chromosome 2q21; region of chromosome Xp11.4, including UPS9X; LOC221829 ; U3 small nuclear RNA; integrin, beta 1 (ITGB1) ; acrosomal vesicle protein 1 (ACRV1) and CHK1 checkpoint homolog (CHEK1); prospero-related homeobox 1 (PROX1); FLJ20627 and FLJ12910; PIN2-interacting protein (PINX1) and SRY (sex-determining region Y)-box 7 (SOX7); LOC131920; region of chromosome 13q14; neurotrophic tyrosine kinase, receptor, type 3 (NTRK3); TERA protein and FLJ13224; LOC284260; POM (POM121 homolog) and ZP3 fusion (POMZP3); DEAD/H box polypeptide 8 (DDX8) and similar to ribosomal protein L29 (cell surface heparin binding protein HIP) (LOC284064); LOC345307 and UDP-N-acetyl-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNT7); Mus musculus 5S rRNA pseudogene (Rn5s-ps1); ribosomal protein L27a pseudogene (RPL27AP) and v-myb myeloblastosis viral oncogene homolog-like 2 (MYBL2); Down's syndrome cell adhesion molecule like 1 (DSCAML1); LOC148529;

Huntingtin-associated protein interacting protein (HAPIP); LOC158525 and similar to RIKEN cDNA 1210001E11 (LOC347366); hypothetical protein FLJ12910; LOC350411; allograft inflammatory factor 1 (AIF1) and HLA-B associated transcript 2 (BAT2); C10orf7; LOC346658 and LOC340349; region of chromosome 12q21; LOC339248 and FLJ22659; SR rich protein DKFZp564B0769 and hypothetical protein MGC14793; FLJ10439; cytochrome P450, family 11, subfamily A, polypeptide 1 (CYP11A1) and sema domain, immunoglobulin domain (Ig) and GPI membrane anchor, (semaphoring) 7A; ribosomal protein S16 (RPS16); hypothetical protein DKFZp434H0115 and ATP citrate lyase (ACLY); calnexin (CANX); protein tyrosine phosphatase, receptor type, K (PTPRK); cyclin M2 (CNNM2); or AXL receptor tyrosine kinase.

13. The method of claim 12, wherein the method comprises interfering with an activity or expression of more than one of the host proteins.

14. The method of claim 12, wherein the method comprises interfering with expression of one or more of the host nucleic acids.

15. The method of claim 6, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising at least 90% identity to any target nucleic acid sequence associated with SEQ ID NOS: 1-35.

16. The method of claim 6, wherein one or more host proteins is encoded by one or more nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS: 1-35.

17. The method of claim 9, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising at least 90% identity to any of SEQ ID NOS: 36-63 or a coding sequence of any of SEQ ID NOS: 36-63.

18. The method of claim 9, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS: 36-63.

19. The method of claim 12, wherein the one or more host proteins are encoded by one or more nucleic acid sequences comprising at least 90% identity to any target nucleic acid sequence associated with SEQ ID NOS: 64-227, 229, and 231.

20. The method of claim 12, wherein one or more host proteins are encoded by one or more nucleic acid sequences comprising any target nucleic acid sequence associated with SEQ ID NOS: 64-227, 229, and 231.

21. The method of claim 1, wherein interfering with the activity of the one or more host proteins comprises decreasing an interaction of a viral protein and the one or more host proteins by disrupting or decreasing expression of the one or more host proteins.

22. The method of claim 21, wherein the viral protein comprises a virus and decreasing the interaction of the viral protein and the one or more host proteins decreases or inhibits infection of a host cell by the virus.

23. The method of claim 21, wherein disrupting or decreasing expression of the host protein comprises disrupting or decreasing transcription of an mRNA encoding the host protein.

24. The method of claim 23, wherein disrupting or decreasing transcription of the mRNA comprises inserting a transposon or insertional vector into a coding region of the nucleic acid encoding the host protein.

25. The method of claim 23, wherein disrupting or decreasing the transcription of the mRNA comprises contacting the mRNA with an antisense RNA, RNAi, ribozyme, or siRNA that recognizes the mRNA.

26. The method of claim 1 wherein interfering with the activity of the host protein comprises decreasing an interaction of a viral protein and the host protein by contacting the cell with an agent that decreases or inhibits the activity or expression of the host protein or that disrupts expression of the host protein.

27. The method of claim 26, wherein the host cell is present in a host subject and wherein contacting the cell with the agent comprises administering the agent to the subject.

28. The method of claim 1, wherein the host cell is a mammalian host cell.

29. A method of decreasing HIV, Ebola, or influenza A infection of a host cell, comprising, decreasing an interaction between a viral nucleic acid and a host nucleic acid by decreasing the integration of the viral nucleic acid into the host nucleic acid, wherein the host nucleic acid comprises at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

30. The method of claim 29, wherein the viral nucleic acid comprises a viral genome and the host nucleic acid comprises a host genome.

31. A method of treating an HIV, Ebola, or influenza A viral infection in a host subject, comprising administering to a subject having a viral infection an effective amount of an agent that interferes with the interaction of a virus and host protein, wherein the host protein is encoded by a nucleic acid comprising at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

32. The method of claim 31, wherein the agent disrupts expression of the nucleic acid encoding the host protein.

33. The method of claim 32, wherein the agent is an antisense, ribozyme, or siRNA molecule that recognizes the nucleic acid sequence comprising at least 90% identity to any target sequence associated with SEQ ID NOS: 1-227, 229, and 231.

34. The method of claim 31, wherein the effective amount induces a prophylactic effect in the host, which inhibits infection of the host by a virus.

35. The method of claim 31, wherein the host was previously infected by a virus and the effective amount induces a therapeutic effect in the host.

36. A method of determining resistance or susceptibility to viral infection in a subject, comprising comparing a first nucleic acid sequence of a subject to a second nucleic acid sequence comprising any target sequence associated with SEQ ID NOS: 1-227, 229, and 231, wherein a higher similarity between the first and second nucleic acid sequence indicates the subject is more susceptible to viral infection, and wherein a lesser similarity between the first and second nucleic acid sequence indicates the subject is more resistant to viral infection.

37. The method of claim 36, wherein the first nucleic acid sequence is obtained from a biological sample of the subject.

38. The method of claim 37, wherein the first nucleic acid sequence comprises a plurality of nucleic acid sequences, wherein each nucleic acid sequence is obtained from a different subject.

39. The method according to claim 36, further comprising determining a polymorphic variation within a population.

40. A method of decreasing HIV, Ebola, or influenza A infection of a host cell, comprising:

contacting the host cell with an anti-protein binding agent that selectively or specifically binds to a host protein encoded by any target sequence associated with SEQ ID NOS: 1-227, 229, and 231 or a protein sequence shown in any of SEQ ID NOS: 228, 230, or 232, wherein the anti-protein

binding agent inhibits an interaction between the host protein and the HIV, Ebola, or influenza A virus.

41. The method of claim 40, wherein the host cell is present in a subject, and contacting the host cell with the anti-protein binding agent comprises administering the anti-protein binding agent to the subject.

42. The method of claim 40, wherein the anti-protein binding agent is an antibody or chemical compound.

43. A method of identifying a compound that decreases binding of a viral protein to a host protein and decreases viral infection, comprising:

contacting the host protein with the viral protein and a test compound, wherein the host protein is a protein in Table 1, and the viral protein is an HIV, Ebola, or influenza A protein; and

determining whether binding of the viral protein to the host protein is decreased in the presence of the test compound, the decrease in binding being an indication that the test compound decreases the binding of viral protein to the target protein, and decreases viral infection.

44. The method of claim 43, wherein the viral protein comprises a virus.

45. The method of claim 43, wherein the viral protein is a viral envelope protein.

46. The method of claim 43, wherein the viral protein is an HIV protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 1-35.

47. The method of 43, wherein the viral protein is an influenza A protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 36-63.

48. The method of claim 43, wherein the viral protein is an Ebola protein and the host protein is a protein encoded by a target sequence associated with SEQ ID NOS: 64-227, 229, and 231.

49. The method of claim 43, wherein the method comprises expressing the host protein in a cell, and contacting the host protein with the viral protein and a test compound comprises exposing the cell to the viral protein and the test compound.

50. The method of claim 43, wherein the host protein or the viral protein comprises a label, and determining whether binding is decreased comprises detecting an amount of label present.

51. A method of decreasing infection of a host cell by a pathogen, comprising interfering with an activity or expression of a Rab9 in the host cell, wherein interfering with Rab9 activity or expression decreases infection of the host cell by the pathogen.

52. The method of claim 51, wherein the pathogen hijacks a lipid raft.

53. The method of claim 51, wherein the pathogen is a *Campylobacter jujuni*, *Vibrio cholerae*, SV40, *Legionella pneumophila*, *Aeromonas hydrophilia*, Echovirus 1, Echovirus 11, *Brucella* spp, *Clostridium* spp., Avian sarcoma and leukosis virus, FimH, Dr *Escherichia coli*, *Streptcoccus pyogenes*, Semiliki forest virus, *Salmonella typhimurium*, *Bacillus anthracis*, Ecotropic mouse leukaemia virus, *Shigella flexneri*, *Bacillus thuringiensis*, HTLV-1, *Chlamydia* spp., *Helicobacter pylori*, HIV-1, *Mycobacterium* spp., *Lysteria monocytogenes*, *Ebola*, *Marburg*, Measles, Herpes Simplex virus, influenza virus, or Epstein-Barr virus.

54. The method of claim 51, wherein the Rab9 host protein is encoded by a host nucleic acid comprising at least 90% identity to a target sequence associated with any of SEQ ID NOS: 118-119.

55. The method of claim 54, wherein the host nucleic acid comprises a target sequence associated with any of SEQ ID NOS: 118-119.

56. The method of claim 51, wherein interfering with expression of Rab9 comprises disrupting or decreasing transcription of an mRNA encoding the Rab9 protein.

57. The method of claim 56 wherein disrupting or decreasing the transcription of the mRNA comprises contacting the mRNA with an antisense RNA, ribozyme, or siRNA that recognizes the mRNA.

58. The method of claim 57, wherein the siRNA sequence comprises any of SEQ ID NOS: 232-235.

59. The method of claim 57, wherein the host cell is present in a subject, and contacting the mRNA with an antisense RNA, ribozyme, or siRNA that recognizes the mRNA comprises administering the antisense RNA, ribozyme, or siRNA to the subject.

60. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 1-35, wherein the cell has a decreased susceptibility to HIV infection.

61. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 36-63, wherein the cell has a decreased susceptibility to influenza infection.

62. A cell comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 64-232, wherein the cell has a decreased susceptibility to Ebola infection.

63. A cell comprising a functional deletion of a Rab9 gene, wherein the cell has a decreased susceptibility to infection by a pathogen that uses lipid rafts.

64. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 1-35, wherein the mammal has decreased suseptibility to infection by HIV.

65. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 36-63, wherein the mammal has decreased suseptibility to infection by influenza.

66. A non-human transgenic mammal comprising a functional deletion of one or more target sequences associated with any of SEQ ID NOS: 64-232, wherein the mammal has decreased suseptibility to infection by Ebola.

67. A non-human transgenic mammal comprising a functional deletion of a Rab9 gene, wherein the mammal has decreased suseptivlity to infection by a pathogen that uses a lipid raft.

68. The method of claim 1, wherein interfering with an activity of the host nucleic acid comprising administering one or more of SEQ ID NOS: 246- 845 to the host cell.